

## SEQUENCE PROTOCOL

&lt;110&gt; Degussa AG

5 &lt;120&gt; Nucleotide sequences which code for the dead gene

&lt;130&gt; 000557 BT

&lt;140&gt;

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&lt;160&gt; 4

&lt;170&gt; PatentIn Ver. 2.1

15

&lt;210&gt; 1

&lt;211&gt; 2381

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (259) .. (2130)

&lt;223&gt; dead gene

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&lt;400&gt; 1

caggaaaccc cgcagggtga ctcagcatca gctgacttcg ctctcgaaac cccaaccaac 60

actgttgaag atgcaccagc atctgagggt agcgaagaga tcaccagggt tgcggatact 120

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tctgaggacg cgcactctgc agatgcagac aacgcgagca atgtaatcaa tgagaatgag 180

gactcctcgg aagggtgctaa ccagccttca aacgagtcac cctctacgga agccaaatcc 240

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ggcttcgatg cactcgga ctg cca gag cgt gta ctt gac gct gtg cgc aag 291

Met Pro Glu Arg Val Leu Asp Ala Val Arg Lys  
1 5 10

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gtg ggt tac gaa act cct tcc cca att cag gca caa acc atc cca atc 339  
Val Gly Tyr Glu Thr Pro Ser Pro Ile Gln Ala Gln Thr Ile Pro Ile  
15 20 25

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ctc atg gag ggc cag gat gtt gtt ggt cta gca cag acc ggt acc ggt 387  
Leu Met Glu Gly Gln Asp Val Val Gly Leu Ala Gln Thr Gly Thr Gly  
30 35 40

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aag act gca gct ttc gcg ctg cca atc ctt gcc cgt att gac aag tcc 435  
Lys Thr Ala Ala Phe Ala Leu Pro Ile Leu Ala Arg Ile Asp Lys Ser  
45 50 55gtg cgc agc cca cag gca ctt gtg ctt gcc cct acc cgt gag cag gca 483  
Val Arg Ser Pro Gln Ala Leu Val Leu Ala Pro Thr Arg Glu Gln Ala  
60 65 70 75

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ctt cag gtt gct gac tcc ttc caa tcc ttc gct gac cac gtc ggt ggc 531  
Leu Gln Val Ala Asp Ser Phe Gln Ser Phe Ala Asp His Val Gly Gly  
80 85 90

ctg aac gtt ctg cca atc tat ggt gga cag gct tac ggc att cag ctc 579  
 Leu Asn Val Leu Pro Ile Tyr Gly Gly Gln Ala Tyr Gly Ile Gln Leu  
 95 100 105

5 tct ggc ctg cgt cgt ggc gct cac atc gtc gtg ggt acc cca ggc cga 627  
 Ser Gly Leu Arg Arg Gly Ala His Ile Val Val Gly Thr Pro Gly Arg  
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10 atc atc gat cac ctc gaa aag ggc tcc ctg gat atc tcc gga ctg cgc 675  
 Ile Ile Asp His Leu Glu Lys Gly Ser Leu Asp Ile Ser Gly Leu Arg  
 125 130 135

15 ttc ctc gtg ctc gat gaa gca gac gag atg ctg aac atg ggc ttc cag 723  
 Phe Leu Val Leu Asp Glu Ala Asp Glu Met Leu Asn Met Gly Phe Gln  
 140 145 150 155

20 gaa gat gtc gag cgc atc ctc gag gac acc cca gac gag aag cag gtt 771  
 Glu Asp Val Glu Arg Ile Leu Glu Asp Thr Pro Asp Glu Lys Gln Val  
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gca cta ttc tcc gca acg atg cca aac ggc att cgt cgc ctg tcc aag 819  
 Ala Leu Phe Ser Ala Thr Met Pro Asn Gly Ile Arg Arg Leu Ser Lys  
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25 cag tac ctg aac aac cct gct gaa atc acc gtt aag tcc gag acc agg 867  
 Gln Tyr Leu Asn Asn Pro Ala Glu Ile Thr Val Lys Ser Glu Thr Arg  
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30 act aac acc aac atc acc cag cgc ttc ctc aac gtt gca cac cgc aac 915  
 Thr Asn Thr Asn Ile Thr Gln Arg Phe Leu Asn Val Ala His Arg Asn  
 205 210 215

35 aag atg gat gca ctg acc cgt att ctc gag gtc acc gag ttt gaa gca 963  
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40 atg atc atg ttc gtg cgc acc aag cac gaa act gaa gaa gtt gct gaa 1011  
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aag ctc cgt gca cgc gga ttc tcc gca gca gcc atc aac ggc gac att 1059  
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45 gct cag gca cag cgt gag cgc acc gtc gac cag ctg aag gac ggc cgc 1107  
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50 ctg gac atc ctc gtt gca acc gac gtt gca gcc cgt ggt ctt gac gtt 1155  
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55 gag cgc atc tcc cac gtg ctt aac ttc gac att cca aac gac acc gag 1203  
 Glu Arg Ile Ser His Val Leu Asn Phe Asp Ile Pro Asn Asp Thr Glu  
 300 305 310 315

tcc tac gtt cac cgc atc ggc cgc acc ggc cgt gca gga cgt acc ggc 1251  
 Ser Tyr Val His Arg Ile Gly Arg Thr Gly Arg Ala Gly Arg Thr Gly  
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gag gca atc ctg ttc gtg acc cca cgt gag cgt cgt atg ctt cgc tcc 1299  
 Glu Ala Ile Leu Phe Val Thr Pro Arg Glu Arg Arg Met Leu Arg Ser  
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 5 atc gag cgc gca acc aac gca cca ctg cac gaa atg gaa ctg cca acc 1347  
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 10 gtc gat cag gtc aac gac ttc cgc aag gtc aag ttc gct gac tcc atc 1395  
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 365 370 375  
 15 acc aag tcc ctc gag gac aag cag atg gac ctg ttc cgc acc ctg gtc 1443  
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 380 385 390 395  
 20 aag gaa tac tcc cag gcc aac gac gtt cct cta gag gac atc gca gcg 1491  
 Lys Glu Tyr Ser Gln Ala Asn Asp Val Pro Leu Glu Asp Ile Ala Ala  
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 25 gca ctg gca acc cag gca cag tcc ggc gac ttc ctg ctc aag gag ctc 1539  
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 415 420 425  
 30 cca cca gag cgc cgt gag cgc aac gac cgc cgt cgt gac cgt gac ttc 1587  
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 35 gac gac cgt ggt gga cgt gga cgc gac cgt gac cgt ggc gac cgc gga 1635  
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 445 450 455  
 40 gat cgt ggc tca cgc ttc gac cgc gac gac gag aac ctg gca acc tac 1683  
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 45 cgc ctc gca gtg ggc aag cgc cag cac atc cgc cca ggc gca atc gtt 1731  
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 50 ggt gca ctt gcc aac gaa ggt ggc ctg aac tcc aag gac ttc ggc cgc 1779  
 Gly Ala Leu Ala Asn Glu Gly Gly Leu Asn Ser Lys Asp Phe Gly Arg  
 495 500 505  
 55 atc acc atc gca gcc gac cac acc ctg gtt gaa ctg cca aag gat ctc 1827  
 Ile Thr Ile Ala Ala Asp His Thr Leu Val Glu Leu Pro Lys Asp Leu  
 510 515 520  
 50 cca cag agc gtt ctt gac aac ctg cgc gac acc cgc atc tcc ggc cag 1875  
 Pro Gln Ser Val Leu Asp Asn Leu Arg Asp Thr Arg Ile Ser Gly Gln  
 525 530 535  
 55 ctc atc aac ata gaa cgc gac tcc ggt gga cgc cca cca cgc cgc ttc 1923  
 Leu Ile Asn Ile Glu Arg Asp Ser Gly Gly Arg Pro Pro Arg Arg Phe  
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gag cgc gat gac cgt ggc gga cgc ggc gga ttc cgc ggc gac cgt gat 1971  
 Glu Arg Asp Asp Arg Gly Gly Arg Gly Gly Phe Arg Gly Asp Arg Asp  
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5 gac cgc ggt gga cgt gga cgt gac cgt gac gat cgt gga agc cgt gga 2019  
 Asp Arg Gly Gly Arg Gly Arg Asp Arg Asp Asp Arg Gly Ser Arg Gly  
 575 580 585

10 ggt ttc cgc ggt gga cgt gac cgt gat gat cgt ggc gga cgc ggt gga 2067  
 Gly Phe Arg Gly Gly Arg Asp Arg Asp Asp Arg Gly Gly Arg Gly Gly  
 590 595 600

15 ttc cgc gga cgc gac gac cgc gga gac cgt ggt ggc cgt ggc ggt tac 2115  
 Phe Arg Gly Arg Asp Asp Arg Gly Asp Arg Gly Arg Gly Gly Tyr  
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cgt ggc gga cgc gac taagagttcg ttttagcttc agctcagggtt ttcgcctgag 2170  
 Arg Gly Gly Arg Asp  
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20 tctggtgctt agctagaaaa atccgttgct ctctctttac tgagagggca acggattttt 2230

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25 gaagtaa atg atggtgcttc gaccgcagca ccatcgtaa gattctgacc aaagaagaga 2350

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Asp Val Val Gly Leu Ala Gln Thr Gly Thr Gly Lys Thr Ala Ala Phe  
 35 40 45

45 Ala Leu Pro Ile Leu Ala Arg Ile Asp Lys Ser Val Arg Ser Pro Gln  
 50 55 60

Ala Leu Val Leu Ala Pro Thr Arg Glu Gln Ala Leu Gln Val Ala Asp  
 65 70 75 80

50 Ser Phe Gln Ser Phe Ala Asp His Val Gly Gly Leu Asn Val Leu Pro  
 85 90 95

55 Ile Tyr Gly Gly Gln Ala Tyr Gly Ile Gln Leu Ser Gly Leu Arg Arg  
 100 105 110

Gly Ala His Ile Val Val Gly Thr Pro Gly Arg Ile Ile Asp His Leu  
 115 120 125

Glu Lys Gly Ser Leu Asp Ile Ser Gly Leu Arg Phe Leu Val Leu Asp  
 130 135 140  
 5 Glu Ala Asp Glu Met Leu Asn Met Gly Phe Gln Glu Asp Val Glu Arg  
 145 150 155 160  
 Ile Leu Glu Asp Thr Pro Asp Glu Lys Gln Val Ala Leu Phe Ser Ala  
 165 170 175  
 10 Thr Met Pro Asn Gly Ile Arg Arg Leu Ser Lys Gln Tyr Leu Asn Asn  
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 Pro Ala Glu Ile Thr Val Lys Ser Glu Thr Arg Thr Asn Thr Asn Ile  
 195 200 205  
 15 Thr Gln Arg Phe Leu Asn Val Ala His Arg Asn Lys Met Asp Ala Leu  
 210 215 220  
 20 Thr Arg Ile Leu Glu Val Thr Glu Phe Glu Ala Met Ile Met Phe Val  
 225 230 235 240  
 Arg Thr Lys His Glu Thr Glu Glu Val Ala Glu Lys Leu Arg Ala Arg  
 245 250 255  
 25 Gly Phe Ser Ala Ala Ala Ile Asn Gly Asp Ile Ala Gln Ala Gln Arg  
 260 265 270  
 Glu Arg Thr Val Asp Gln Leu Lys Asp Gly Arg Leu Asp Ile Leu Val  
 275 280 285  
 30 Ala Thr Asp Val Ala Ala Arg Gly Leu Asp Val Glu Arg Ile Ser His  
 290 295 300  
 Val Leu Asn Phe Asp Ile Pro Asn Asp Thr Glu Ser Tyr Val His Arg  
 305 310 315 320  
 35 Ile Gly Arg Thr Gly Arg Ala Gly Arg Thr Gly Glu Ala Ile Leu Phe  
 325 330 335  
 40 Val Thr Pro Arg Glu Arg Arg Met Leu Arg Ser Ile Glu Arg Ala Thr  
 340 345 350  
 Asn Ala Pro Leu His Glu Met Glu Leu Pro Thr Val Asp Gln Val Asn  
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 45 Asp Phe Arg Lys Val Lys Phe Ala Asp Ser Ile Thr Lys Ser Leu Glu  
 370 375 380  
 Asp Lys Gln Met Asp Leu Phe Arg Thr Leu Val Lys Glu Tyr Ser Gln  
 385 390 395 400  
 Ala Asn Asp Val Pro Leu Glu Asp Ile Ala Ala Ala Leu Ala Thr Gln  
 405 410 415  
 55 Ala Gln Ser Gly Asp Phe Leu Leu Lys Glu Leu Pro Pro Glu Arg Arg  
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 Glu Arg Asn Asp Arg Arg Arg Asp Arg Asp Phe Asp Asp Arg Gly Gly  
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Arg Gly Arg Asp Arg Asp Arg Gly Asp Arg Gly Asp Arg Gly Ser Arg  
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 5 Phe Asp Arg Asp Asp Glu Asn Leu Ala Thr Tyr Arg Leu Ala Val Gly  
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 Lys Arg Gln His Ile Arg Pro Gly Ala Ile Val Gly Ala Leu Ala Asn  
 485 490 495  
 10 Glu Gly Gly Leu Asn Ser Lys Asp Phe Gly Arg Ile Thr Ile Ala Ala  
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 Asp His Thr Leu Val Glu Leu Pro Lys Asp Leu Pro Gln Ser Val Leu  
 515 520 525  
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 530 535 540  
 Arg Asp Ser Gly Gly Arg Pro Pro Arg Arg Phe Glu Arg Asp Asp Arg  
 545 550 555 560  
 Gly Gly Arg Gly Gly Phe Arg Gly Asp Arg Asp Asp Arg Gly Gly Arg  
 565 570 575  
 20 Gly Arg Asp Arg Asp Asp Arg Gly Ser Arg Gly Gly Phe Arg Gly Gly  
 580 585 590  
 Arg Asp Arg Asp Asp Arg Gly Gly Arg Gly Gly Phe Arg Gly Arg Asp  
 595 600 605  
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 <212> DNA  
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 int2

